

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☐

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

HTHQDFQPVHLHLVALNTPLS



Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

ISSANYEKPALHLAALNMPFSGDIRADFQCFKQARAAGLLSTYRAFLSSHLDL
STIVRKAERYSLPIVNLKGQVLFNNWDSIFSGHGGQFNMHIPIYSFDGRDIMTD
PSWPQKVIWHGSSPHGVRLVDNYCEAWRTADTAVTGLASPLSTGKILDQKAYSC
ANRLIVLCIENSFMTDARK



Comments and suggestions to: blast-help@ncbi.nlm.nih.gov

Credits to: [Tatiana Tatusov](#) and [Tom Madden](#)

EXHIBIT

6-1



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0 wordsize: 3 [Filter](#)

Sequence 1 lc|seq_1 Length 20

Sequence 2 lc|seq_2 Length 181

No significant similarity was found

